STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

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Application Serial Number: _10/579,879_
Source: _IFWP_
Date Processed by STIC: _5-31-06_

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Revised 01/10/06
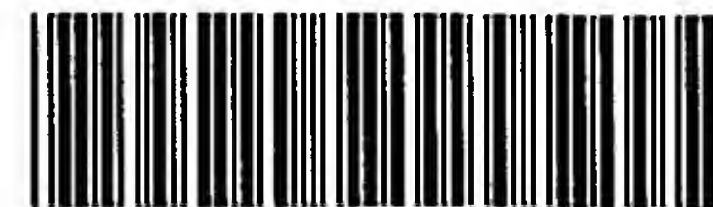
IFWP

RAW SEQUENCE LISTING   DATE: 05/31/2006
PATENT APPLICATION: **US/10/579,879**   TIME: 13:23:45

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF4\05312006\J579879.raw**

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 3 <110> APPLICANT: The Government of the United States of America, as
 4       represented by the Secretary of the Department of Health and
 5       Human Services
 6       Flomerfelt, Francis
 7       Gress, Ronald
 9 <120> TITLE OF INVENTION: SPATIAL FOR ALTERING CELL PROLIFERATION
11 <130> FILE REFERENCE: 4239-64851-02
13 <140> CURRENT APPLICATION NUMBER: US/10/579,879
13 <141> CURRENT FILING DATE: 2006-05-17
13 <150> PRIOR APPLICATION NUMBER: PCT/US2003/036874
14 <151> PRIOR FILING DATE: 2003-11-18
16 <160> NUMBER OF SEQ ID NOS: 7
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 933
22 <212> TYPE: DNA
23 <213> ORGANISM: Mus musculus
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (84)..(677)
29 <223> OTHER INFORMATION: Coding sequence
31 <400> SEQUENCE: 1
32 tcttgaggtt gccaattttt tttttttttt tttttttttt tttttttttt ggtttgggga      60
34 gaaacttgtg ttggaaccag ccc ctg ttt ctg ggg aat gta tat aag ggg agt     113
35                       Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser
36                        1                5                   10
38 tta gca cct cgt agg gat gag gtg act agt cca aag gca gag ccc cag        161
39 Leu Ala Pro Arg Arg Asp Glu Val Thr Ser Pro Lys Ala Glu Pro Gln
40            15                  20                  25
42 cca gag acg aag ccg gag aac ctt cca agg agc cac ggg gat gtt ggg        209
43 Pro Glu Thr Lys Pro Glu Asn Leu Pro Arg Ser His Gly Asp Val Gly
44            30                  35                  40
46 ctc cag aaa gag act gtg gtc cca ggc att gtg gat ttc gag ctg atc        257
47 Leu Gln Lys Glu Thr Val Val Pro Gly Ile Val Asp Phe Glu Leu Ile
48            45                  50                  55
50 cat gag gag ctg aag acc aca aag ccc caa aca tca caa cca aca ccc        305
51 His Glu Glu Leu Lys Thr Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro
52     60                  65                  70
54 agt gcc tac cgc ttt gga cgc cta agc cac cat tcc ttc ttc tcg agg        353
55 Ser Ala Tyr Arg Phe Gly Arg Leu Ser His His Ser Phe Phe Ser Arg
56 75                  80                  85                  90
58 cac cac ccc caa cca cag cga gtg act cat atc caa gat atc gct ggg        401
59 His His Pro Gln Pro Gln Arg Val Thr His Ile Gln Asp Ile Ala Gly
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RAW SEQUENCE LISTING   DATE: 05/31/2006
PATENT APPLICATION: **US/10/579,879**   TIME: 13:23:45

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF4\05312006\J579879.raw**

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60                 95               100              105
62 aag cct gtc tgc gtg gtc agg gac gag ttc tct ctg tcg gcc ttg act    449
63 Lys Pro Val Cys Val Val Arg Asp Glu Phe Ser Leu Ser Ala Leu Thr
64         110              115              120
66 cag ccc aca ttc tta tcc cgc tgt ctg atg ggg atg ccc acc atc tct    497
67 Gln Pro Thr Phe Leu Ser Arg Cys Leu Met Gly Met Pro Thr Ile Ser
68         125              130              135
70 gtc ccc att ggg gat cca cag tcc aat cgg aac ccc cag ctt tct act    545
71 Val Pro Ile Gly Asp Pro Gln Ser Asn Arg Asn Pro Gln Leu Ser Thr
72         140              145              150
74 tct gac acc tgg agg aag aaa ctg aag gac ctg gct tcc cga gtg act    593
75 Ser Asp Thr Trp Arg Lys Lys Leu Lys Asp Leu Ala Ser Arg Val Thr
76 155              160              165              170
78 gtc ttc act aag gaa atc cag cca aag ccc gat gag gtt ggt gtt gca    641
79 Val Phe Thr Lys Glu Ile Gln Pro Lys Pro Asp Glu Val Gly Val Ala
80         175              180              185
82 caa aga atg gag cct aga aaa aaa agg cct tct taa gtctccccaa         687
83 Gln Arg Met Glu Pro Arg Lys Lys Arg Pro Ser
84         190              195
86 tgctcagctg ctggcacggg aggggaagga ccctcataac ctcgaaggtg acagcgaaaa  747
88 tcaaagaaac acaaatcac acctagcaga gaaatccaag aagggttccc agaaacaccc    807
90 tctaaagcaa ctgttcccaa cctgtctaat gccttgaccc ttgaatacag tttctcacac  867
92 tgcagtaacc cctgcccccg aaataaaatt attttcatta ctacttcaaa aaaaaaaaa   927
94 aaaaaa                                                            933
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 197
99 <212> TYPE: PRT
100 <213> ORGANISM: Mus musculus
102 <400> SEQUENCE: 2
104 Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser Leu Ala Pro Arg Arg Asp
105 1             5               10              15
108 Glu Val Thr Ser Pro Lys Ala Glu Pro Gln Pro Glu Thr Lys Pro Glu
109         20              25              30
112 Asn Leu Pro Arg Ser His Gly Asp Val Gly Leu Gln Lys Glu Thr Val
113         35              40              45
116 Val Pro Gly Ile Val Asp Phe Glu Leu Ile His Glu Glu Leu Lys Thr
117     50              55              60
120 Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro Ser Ala Tyr Arg Phe Gly
121 65              70              75              80
124 Arg Leu Ser His His Ser Phe Phe Ser Arg His His Pro Gln Pro Gln
125         85              90              95
128 Arg Val Thr His Ile Gln Asp Ile Ala Gly Lys Pro Val Cys Val Val
129         100              105              110
132 Arg Asp Glu Phe Ser Leu Ser Ala Leu Thr Gln Pro Thr Phe Leu Ser
133         115              120              125
136 Arg Cys Leu Met Gly Met Pro Thr Ile Ser Val Pro Ile Gly Asp Pro
137     130              135              140
140 Gln Ser Asn Arg Asn Pro Gln Leu Ser Thr Ser Asp Thr Trp Arg Lys
141 145             150             155             160
```

```
144 Lys Leu Lys Asp Leu Ala Ser Arg Val Thr Val Phe Thr Lys Glu Ile
145               165                 170                 175
148 Gln Pro Lys Pro Asp Glu Val Gly Val Ala Gln Arg Met Glu Pro Arg
149               180                 185                 190
152 Lys Lys Arg Pro Ser
153               195
156 <210> SEQ ID NO: 3
157 <211> LENGTH: 1035
158 <212> TYPE: DNA
159 <213> ORGANISM: Mus musculus
162 <220> FEATURE:
163 <221> NAME/KEY: CDS
164 <222> LOCATION: (84)..(779)
165 <223> OTHER INFORMATION: Coding sequence
167 <400> SEQUENCE: 3
168 tcttgaggtt gccaattttt tttttttttt tttttttttt tttttttttt ggtttgggga     60
170 gaaacttgtg ttggaaccag ccc ctg ttt ctg ggg aat gta tat aag ggg agt    113
171                         Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser
172                          1                 5                 10
174 tta gca cct cgt agg gat gag gtg act agt cca aag gca gag ccc cag     161
175 Leu Ala Pro Arg Arg Asp Glu Val Thr Ser Pro Lys Ala Glu Pro Gln
176               15                  20                  25
178 cca gag acg aag ccg gag aac ctt cca agg agc cac ggg gat gtt ggg     209
179 Pro Glu Thr Lys Pro Glu Asn Leu Pro Arg Ser His Gly Asp Val Gly
180               30                  35                  40
182 ctc cag aaa gag act gtg gtc cca ggc att gtg gat ttc gag ctg atc     257
183 Leu Gln Lys Glu Thr Val Val Pro Gly Ile Val Asp Phe Glu Leu Ile
184               45                  50                  55
186 cat gag gag ctg aag acc aca aag ccc caa aca tca caa cca aca ccc     305
187 His Glu Glu Leu Lys Thr Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro
188       60                  65                  70
190 agt gcc tac cgc ttt gga cgc cta agc cac cat tcc ttc ttc tcg agg     353
191 Ser Ala Tyr Arg Phe Gly Arg Leu Ser His His Ser Phe Phe Ser Arg
192 75                  80                  85                  90
194 cac cac ccc caa cca cag cga gtg act cat atc caa gtt aca gga aga     401
195 His His Pro Gln Pro Gln Arg Val Thr His Ile Gln Val Thr Gly Arg
196               95                  100                 105
198 gag gac ctg gag cac tcc ctg ccc ctc acc acc tct ttc cag ctc ctt     449
199 Glu Asp Leu Glu His Ser Leu Pro Leu Thr Thr Ser Phe Gln Leu Leu
200               110                 115                 120
202 caa gct cct ggg gtc cag ccc atg gat ctc act ccc tct gca gat atc     497
203 Gln Ala Pro Gly Val Gln Pro Met Asp Leu Thr Pro Ser Ala Asp Ile
204               125                 130                 135
206 gct ggg aag cct gtc tgc gtg gtc agg gac gag ttc tct ctg tcg gcc     545
207 Ala Gly Lys Pro Val Cys Val Val Arg Asp Glu Phe Ser Leu Ser Ala
208       140                 145                 150
210 ttg act cag ccc aca ttc tta tcc cgc tgt ctg atg ggg atg ccc acc     593
211 Leu Thr Gln Pro Thr Phe Leu Ser Arg Cys Leu Met Gly Met Pro Thr
212 155                 160                 165                 170
```

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF4\05312006\J579879.raw**

```
214 atc tct gtc ccc att ggg gat cca cag tcc aat cgg aac ccc cag ctt    641
215 Ile Ser Val Pro Ile Gly Asp Pro Gln Ser Asn Arg Asn Pro Gln Leu
216                 175                 180                 185
218 tct act tct gac acc tgg agg aag aaa ctg aag gac ctg gct tcc cga    689
219 Ser Thr Ser Asp Thr Trp Arg Lys Lys Leu Lys Asp Leu Ala Ser Arg
220                 190                 195                 200
222 gtg act gtc ttc act aag gaa atc cag cca aag ccc gat gag gtt ggt    737
223 Val Thr Val Phe Thr Lys Glu Ile Gln Pro Lys Pro Asp Glu Val Gly
224             205                 210                 215
226 gtt gca caa aga atg gag cct aga aaa aaa agg cct tct taa            779
227 Val Ala Gln Arg Met Glu Pro Arg Lys Lys Arg Pro Ser
228         220                 225                 230
230 gtctccccaa tgctcagctg ctggcacggg aggggaagga ccctcataac ctcgaaggtg    839
232 acagcgaaaa tcaaagaaac acaaaatcac acctagcaga gaaatccaag aagggttccc    899
234 agaaacaccc tctaaagcaa ctgttcccaa cctgtctaat gccttgaccc ttgaatacag    959
236 tttctcacac tgcagtaacc cctgcccccg aaataaaatt attttcatta ctacttcaaa   1019
238 aaaaaaaaaa aaaaaa                                                   1035
241 <210> SEQ ID NO: 4
242 <211> LENGTH: 231
243 <212> TYPE: PRT
244 <213> ORGANISM: Mus musculus
246 <400> SEQUENCE: 4
248 Leu Phe Leu Gly Asn Val Tyr Lys Gly Ser Leu Ala Pro Arg Arg Asp
249 1               5                   10                  15
252 Glu Val Thr Ser Pro Lys Ala Glu Pro Gln Pro Glu Thr Lys Pro Glu
253                 20                  25                  30
256 Asn Leu Pro Arg Ser His Gly Asp Val Gly Leu Gln Lys Glu Thr Val
257             35                  40                  45
260 Val Pro Gly Ile Val Asp Phe Glu Leu Ile His Glu Glu Leu Lys Thr
261     50                  55                  60
264 Thr Lys Pro Gln Thr Ser Gln Pro Thr Pro Ser Ala Tyr Arg Phe Gly
265 65                  70                  75                  80
268 Arg Leu Ser His His Ser Phe Phe Ser Arg His His Pro Gln Pro Gln
269                 85                  90                  95
272 Arg Val Thr His Ile Gln Val Thr Gly Arg Glu Asp Leu Glu His Ser
273                 100                 105                 110
276 Leu Pro Leu Thr Thr Ser Phe Gln Leu Leu Gln Ala Pro Gly Val Gln
277             115                 120                 125
280 Pro Met Asp Leu Thr Pro Ser Ala Asp Ile Ala Gly Lys Pro Val Cys
281     130                 135                 140
284 Val Val Arg Asp Glu Phe Ser Leu Ser Ala Leu Thr Gln Pro Thr Phe
285 145                 150                 155                 160
288 Leu Ser Arg Cys Leu Met Gly Met Pro Thr Ile Ser Val Pro Ile Gly
289             165                 170                 175
292 Asp Pro Gln Ser Asn Arg Asn Pro Gln Leu Ser Thr Ser Asp Thr Trp
293             180                 185                 190
296 Arg Lys Lys Leu Lys Asp Leu Ala Ser Arg Val Thr Val Phe Thr Lys
297             195                 200                 205
300 Glu Ile Gln Pro Lys Pro Asp Glu Val Gly Val Ala Gln Arg Met Glu
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RAW SEQUENCE LISTING   DATE: 05/31/2006
PATENT APPLICATION: US/10/579,879   TIME: 13:23:45

        Input Set : A:\Sequence Listing.txt
        Output Set: N:\CRF4\05312006\J579879.raw

```
301     210                 215                 220
304 Pro Arg Lys Lys Arg Pro Ser
305 225                 230
308 <210> SEQ ID NO: 5
309 <211> LENGTH: 2117
310 <212> TYPE: DNA
311 <213> ORGANISM: Mus musculus
314 <220> FEATURE:
315 <221> NAME/KEY: CDS
316 <222> LOCATION: (40)..(1365)
318 <400> SEQUENCE: 5
319 aagaaaagaa ggagaataga ggagctgctg gctgagaaa atg gct gtt gat ggt        54
320                                                 Met Ala Val Asp Gly
321                                                 1                 5
323 ggg tgt ggg gac act gga gac tgg gaa ggt cgc tgg aac cat gta aag     102
324 Gly Cys Gly Asp Thr Gly Asp Trp Glu Gly Arg Trp Asn His Val Lys
325                 10                  15                  20
327 aag ttc ctc gag cgg tct gga ccc ttc aca cac ccc gat ttc gaa cca    150
328 Lys Phe Leu Glu Arg Ser Gly Pro Phe Thr His Pro Asp Phe Glu Pro
329                 25                  30                  35
331 agc act gaa tca ctc cag ttc ttg tta gat aca tgt aaa gtt cta gtc    198
332 Ser Thr Glu Ser Leu Gln Phe Leu Leu Asp Thr Cys Lys Val Leu Val
333                 40                  45                  50
335 att gga gct ggt ggc tta gga tgt gag ctt ctg aaa aat ctg gca tta    246
336 Ile Gly Ala Gly Gly Leu Gly Cys Glu Leu Leu Lys Asn Leu Ala Leu
337             55                  60                  65
339 tct ggt ttt aga cag att cat gtt ata gac atg gac act ata gat gtt    294
340 Ser Gly Phe Arg Gln Ile His Val Ile Asp Met Asp Thr Ile Asp Val
341 70                  75                  80                  85
343 tcc aat tta aat aga cag ttt tta ttt agg cct aaa gat gty gga aga    342
W--> 344 Ser Asn Leu Asn Arg Gln Phe Leu Phe Arg Pro Lys Asp (Xaa) Gly Arg
345                 90                  95                  100
347 ccc aag gct gaa gtt gct gca gaa ttc cta aat gac aga gtt cct aac    390
348 Pro Lys Ala Glu Val Ala Ala Glu Phe Leu Asn Asp Arg Val Pro Asn
349                 105                 110                 115
351 tgc aac gtg gtm cca cat ttc aac aag atw caa gat ttt aac gac act    438
W--> 352 Cys Asn Val (Xaa) Pro His Phe Asn Lys Xaa Gln Asp Phe Asn Asp Thr
353                 120                 125                 130
355 ttc tac cga caa ttt cat atc att gta tgt ggc ctg gac tct atc ata    486
356 Phe Tyr Arg Gln Phe His Ile Ile Val Cys Gly Leu Asp Ser Ile Ile
357             135                 140                 145
359 gcg aga aga tgg atc aat gga atg ctg ata tct ctt cta aat tat gaa    534
360 Ala Arg Arg Trp Ile Asn Gly Met Leu Ile Ser Leu Leu Asn Tyr Glu
361 150                 155                 160                 165
363 gat ggt gtg ttg gat cca agc tcc att gta cct ttg ata gat ggg ggg    582
364 Asp Gly Val Leu Asp Pro Ser Ser Ile Val Pro Leu Ile Asp Gly Gly
365                 170                 175                 180
367 aca gaa ggc ttt aaa ggg aat gcc cga gtg att ttg cct gga atg acc    630
368 Thr Glu Gly Phe Lys Gly Asn Ala Arg Val Ile Leu Pro Gly Met Thr
```

Pls Explain "xqq" locations See pg-6 for Error Explanation

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/31/2006
PATENT APPLICATION: US/10/579,879   TIME: 13:23:46

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF4\05312006\J579879.raw**

Error Explanation.

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 99,121,127,222
Seq#:6; Xaa Pos. 99,121,127,222

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/579,879**

DATE: 05/31/2006
TIME: 13:23:46

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF4\05312006\J579879.raw**

```
L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:344 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:5
L:344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:342
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:438
L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:726
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:96
L:515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:112
L:539 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:208
```